

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

1                   1.       (Previously presented) A method for treating HIV infection in a human  
2 infected with the HIV virus, said method comprising:  
3                   transplanting into the human a stem cell-rich population of cells from a human  
4 donor, wherein the stem cell-rich population of cells has been screened to identify that it has a  
5 beneficial gene that has ~~is~~ a homozygous polymorphism in a CCR5 gene and the encoded CCR5  
6 receptor does not facilitate HIV entry into the immune cell, wherein in the polymorphism is a 32  
7 basepair deletion in the coding region of the CCR5 gene, and wherein the immune cells of the  
8 human are reduced or eliminated prior to transplantation, thereby treating the HIV infection,  
9 wherein HIV entry into the immune cell of the human is facilitated by the CCR5 receptor and  
10 wherein the stem cell-rich population of cells is umbilical cord blood.

2-19   (Canceled)

1                   20.     (Previously presented) The method of claim 1, wherein said method  
2 further comprises identification of the HLA genotype or phenotype of said stem cell-rich  
3 population of cells.

21-23   (Canceled)

1                   24.     (Previously presented) The method of claim 1, further comprising a step  
2 of screening a cell sample from a human donor to identify the stem cell-rich population of cells  
3 that has a polymorphism in the CCR5 gene.

1                   25.     (Previously presented) The method of claim 24, wherein said  
2 polymorphism in the CCR5 gene is detected using a hybridization-based assay, a sequencing  
3 assay, or a functional assay.

26-27 (Canceled)

1                   28.   (Previously presented) The method of claim 24, wherein said method  
2 further comprises

3                   b) identification of an HLA genotype or phenotype of said stem cell-rich  
4 population of cells.

1                   29.   (Previously presented) The method of claim 28, wherein said  
2 identification of the HLA genotype is via a high-throughput method using allele-specific primers  
3 and HLA locus-specific capture oligonucleotides immobilized on a solid phase.

1                   30.   (Previously presented) The method of claim 28, wherein said method  
2 further comprises

3                   c) identification of an HLA genotype or phenotype of said human.

1                   31.   (Previously presented) The method of claim 28, wherein said HLA  
2 genotype or phenotype of said stem cell-rich population of cells is compatible with said HLA  
3 genotype or phenotype of said human.

32.   (Canceled)

1                   33.   (Previously presented) The method of claim 1, wherein multiple samples  
2 of the stem cell-rich populations of cells with the beneficial gene are transplanted into the  
3 human.

1                   34.   (Previously presented) The method of claim 33, wherein the multiple  
2 samples of the stem cell-rich populations of cells with the beneficial gene have an HLA  
3 unmatched genotype or phenotype.